

1

SEQUENCE LISTING

<110> SYNGENTA PARTICIPATIONS AG

<120> EXPRESSION IN PLANTS OF ANTIBODIES AGAINST ENTEROTOXIGENIC ESCHERICHIA COLI

<130> S 70235/WO

<150> US 60/448429

<151> 2003-02-18

<160> 80

<170> PatentIn version 3.1

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K99 codon optimised VH

<400> 1

actagtgagg tgcagctcgt ggagtcgggc ggcggcttcg tgaagccggg cggctccctc	60
aagctctcct gcgccgcctc cggcttcacc ttctccgact acttcatgtc ctggattcgc	120
cagaccccgga gaagcgcct ggagtgggtc gccaccatca acaacggcgg ctcccacacc	180
tactgtctcg acaacgtgaa gggccgcttc accaccttcc gcgacaacgt gaagaacacc	240
ctctacctcc agatgtcctc cctcaacttc gaggacaccg ccatgtacta ctgcgccgcg	300
gcctactacc gcttcgacgt gcgcgcctgg ttctctact ggggccaggg caccctcgtg	360
accgtgtcca cggccaagac caccgcgcg tccgtctac	399

2

<210> 2

<211> 582

<212> DNA

<213> Artificial Sequence

<220>

<223> anti K99 Codon optimised VL

<400> 2

```

agtgacatcc tcctcaccca gtccccggcc atcctctcca tgatcccgcg ccagcgcgtg      60
tcctttctcct gccgcgcctc ccagatcatc ggcaccacca tccactggtc ccagcagcgc      120
accgacggct ccccgcgctt cctcatccag tgcgcctccg agtccatctc cggcatcccg      180
tcccgcttct cgggcaccgg ctccggcacc gacttcaccc tcaacttcaa ctccgtggag      240
tccgagtaca tcaccgacta ctactgccag cagtccaaca cctggccgac ctacccgttc      300
ggcggcgcca ccaagctcga gatcaagcgc gccgacgccg ccccgaccgt gtccatcttc      360
ccgccgtcct ccgagcagct cacctccggc ggcgcgtccg tgggtgtgctt cctcaacaac      420
ttctacccga aggacatcaa cgtgaagtgg aagatcgacg gctccgagcg ccagaacggc      480
gtgctcaact cctggaccga ccaggactcc aaggactcca cctactccat gtccctcacc      540
ctcaccctca ccaaggacga gtacgagcgc cacaactcct ac                          582

```

<210> 3

<211> 399

<212> DNA

<213> Mouse

<400> 3

```

actagtgaag tgcaactggg ggagtctggg ggaggcttcg tgaagcctgg agggtccttg      60
aaactctcct gtgcagcctc tggattcact ttcagtgact atttcatgtc ttggattcgc      120
cagactccgg aaaagaggct ggagtgggtc gcaaccatta ataatgggtg tagtcacacc      180
tactgttcag acaatgtgaa gggacgattt acaactttca gagacaatgt caaaaacacc      240
ctgtaccttc aaatgagcag tctgaacttt gaggacacag ccatgtatta ctgtgcaaga      300
gcctactata ggttcgacgt gagggcctgg ttttcttatt ggggccaaagg gactctggtc      360
actgtctcta cagccaaaac gacaccccca tctgtctac                          399

```

3

<210> 4

<211> 330

<212> DNA

<213> Mouse

<400> 4

```

actagtgaca tcttgctgac tcagtctcca gccatcctgt ctatgattcc aagacaaaga      60
gtcagtttct cctgcagggc cagtcagatc attggcacia ccatacactg gtctcagcaa      120
agaacagatg gttctcctag gcttctcata cagtgtgctt ctgagtctat ctctgggac      180
ccttccaggt ttagtggcac tggatcaggg acagatttta ctcttaactt caacagtgtg      240
gagtctgaat atattacaga ttattactgt caacaaagta atacctggcc aacgtacccg      300
ttcggagggg ggaccaagct cgagataaaa      330

```

<210> 5

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VH from 17_44

<400> 5

```

actagtgacg tgcagctcgt ggagtccggc ggcggcctcg tgcagccggg cggctcccgc      60
aagctctcct gcgcgcctc cggttcacc ttctcctcct tcgccatgca ctgggtgcgc      120
caggccccag agaagggcct ggagtgggtg gctacatct cctccggctc catcaccatc      180
tactacgccg acaccgtgaa gggccgcttc accgtgtccc gcgacaaccc gaagtccacc      240
ctcttcctcc agatgacctc cctccgcagc gaggacaccg ccatgtacta ctgcgcccgc      300
gacgactacg gctcctccgg ctggtacttc gacgtctggg gcgctggcac caggtgacc      360
gtgtcctcgg ccaagaccac cccgccgtcc gtctac      396

```

<210> 6

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VL from 17_44

<400> 6

```
actagtgaca tcgtgatgtc ccagtcctcg tcctccctcg ccgtgtccgc tggcgagaag      60
gtcaccatgt cctgcaagtc ctcccagtc ctccctcaact ccgcacccg caagaactac      120
ctcgccctggt atcagcagaa gccgggccag tccccgaagc tcctcatcta ctgggcctcc      180
acccgcgagt cgggcgtgcc ggaccgcttc accggctccg gctccggcac cgacttcacc      240
ctcaccatct cctccgtgca ggccgaggac ctgcgcgtgt actactgcac ccagtcctac      300
aacctcctca ccttcggcgc cgttaccaag ctcgag                                336
```

<210> 7

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VH from 36_41

<400> 7

```
actagtgagg tccagctgca gcagtctgga cctgaactag tgaagactgg ggcttcagtg      60
aagatatacct gcaaggcttc tgattactca ctactgatt actacatgca ctgggtcaag      120
cagagccatg gagagagcct tgagtggatt ggatatatta atttttacaa tgggtgctact      180
aactacaacc agaagttcaa gggcaaggcc acatttactg tagacacatc ctccagcaca      240
gtctacatgc agttcaacag cctgacatct gaagactctg cggctctatta ttgtgtaaga      300
gaagcattac tacggaacta tgctatggac tactggggtc aaggaacctc agtcaccgtc      360
tcctcagcca aaacgacacc cccatctgtc tac                                393
```

<210> 8

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

5

<223> anti-K88 Codon optimised VL from 36_41

<400> 8
 actagtgtgaaa atgtgtctcac ccagtctcca gcaatcatgt ctgcatctcc aggggaaaag 60
 gtcaccatga cctgcagggc cagctcaagt gtaagttccc gttacttgca ctggtaccag 120
 cagaagtcag gtgcctcccc caaactctgg atttatagca catccaactt ggcttctgga 180
 gtccctgtctc gcttcagtgg cagtgggtct gggacctctt actctctcac aatcagcagt 240
 gtggaggctg aagatgctgc cacttattac tgccagcaat acagtgggta cccgtggacg 300
 ttcggtggag gcaccaagct cgag 324

<210> 9

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VH from 7_46

<400> 9
 actagtgaag tgaagcttga ggagtctgga ggaggcttgg tgcaacctgg aggatccatg 60
 agactctcct gtgttgcttc tggattcact ttcagtaact actggatgaa ctgggtccgc 120
 cagtctccag agaaggggct tgagtgggtt gctgaaatta gattgacatc taataatttt 180
 gcaacacatt atgcggagtc tgtgaaaggg aggttcacca tctcaagaga tgattccaaa 240
 agtagtgtct acctgcaaat gaacaactta agagctgaag aactggcat ttattactgt 300
 accaggcctt actacggtgg taggttcttc tactgggtact tcgatgtctg gggcgcaggg 360
 accacggtca ccgtctctc aacaaaaacg acacccccat ctgtctac 408

<210> 10

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-K88 Codon optimised VL from 7_46

<400> 10
 actagtgtgaaa ttgtgtctcac ccagtctcca accaccatgg ctgcatctcc cggggagaag 60

6

atcactatca cctgcagtgc cagctcaagt ataagttcca attacttgca ttggtatcag	120
cagaagccag gattctcccc taaactcttg atttatagga catccaatct ggcttctgga	180
gtcccagttc gcttcagtgg cagtgggtct gggacctctt actctctcac aattggcacc	240
atggaggctg aagatgttgc cacttactac tgccagcagg gtaatagtat accattcacg	300
ttcggctcgg ggacaaagct cgag	324

<210> 11

<211> 363

<212> DNA

<213> Mouse

<400> 11	
gatgtgcagc tggtggagtc tgggggaggc ttagtgcagc ctggagggtc ccggaaactc	60
tcctgtgcag cctctggatt cactttcagt agctttgcaa tgcactgggt tcgtcaggct	120
ccagagaagg ggctggagtg ggtcgcatat attagtagtg gcagtattac catctactat	180
gcagacacag tgaagggccg attcacctgc tccagagaca atcccaagag caccctgttc	240
ctgcaaataa ccagtctaag gtctgaggac acggccatgt attactgtgc aagagacgac	300
tacggtagta gcgggtggta cttcgatgtc tggggcgagc ggaccacggc caccgtctcc	360
tca	363

<210> 12

<211> 350

<212> DNA

<213> Mouse

<400> 12	
gacattgtga tgtcacagtc tccatcctcc ctggctgtgt cagcaggaga gaaggctcact	60
atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa ctacttggct	120
tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg	180
gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cacyctcacc	240
atcagcagtg tgcaggctga agacctggca gtttattact gcacgcaatc ttataatctg	300
ctcacgttcg gtgctgggac caagctggaa ctgaatcggg ctgatgctgc	350

7

<210> 13

<211> 410

<212> DNA

<213> Mouse

<400> 13

gagggtccagc tgcagcagtc tggacctgaa ctagtgaaga ctggggcttc agtgaagata	60
tcctgcaagg cttctgatta ctcaactact gattactaca tgcactgggt caagcagagc	120
catggagaga gccttgagtg gattggatat attaatTTTT acaatgggtc tactaactac	180
aaccagaagt tcaagggcaa ggccacattt actgtagaca catcctccag cacagtctac	240
atgcagttca acagcctgac atctgaagac tctgcggtct attattgtgt aagagaagca	300
ttactacgga actatgctat ggactactgg ggtcaaggaa cctcagtcac cgtctcctca	360
gccaaaacga cccccccatc tgtctatcca ctggccccta ctagtgctgc	410

<210> 14

<211> 317

<212> DNA

<213> Mouse

<400> 14

gaaaatgtgc tcaccagtc tccagcaatc atgtctgcat ctccagggga aaagggtcacc	60
atgacctgca gggccagctc aagtgtaatg tcccgttact tgcactggta ccagcagaag	120
tcagggtgcct cccccaaact ctggatttat agcacatcca acttggcttc tggagtcctc	180
gctcgcttca gtggcagtggt gtctgggacc tcttactctc tcacaatcag cagtgtggag	240
gctgaagatg ctgccactta ttactgccag caatacagtg gttaccctg gacgttcggt	300
ggaggcacca agctgga	317

<210> 15

<211> 374

<212> DNA

<213> Mouse

<400> 15

gaagtgaagc ttgaggagtc tggaggaggc ttggtgcaac ctggaggatc catgagactc	60
-------------------------------------------------------------------	----

8

ttcctgtgttg cctctggatt cactttcagt aactactgga tgaactgggt ccgccagtct 120
 ccagagaagg ggcttgagtg gggtgctgaa attagattga catctaataa ttttgcaaca 180
 cattatgcgg agtctgtgaa agggagggttc accatctcaa gagatgattc caaaagtagt 240
 gtctacctgc aaatgaacaa cttaagagct gaagacactg gcatttatta ctgtaccagg 300
 ccttactacg gtggtaggtt cttctactgg tacttcgatg tctggggcgc agggaccacg 360
 gtcaccgtct cctc 374

<210> 16

<211> 318

<212> DNA

<213> Mouse

<400> 16

gaaattgtgc tcaccagtc tccaaccacc atggctgcat ctcccgggga gaagatcact 60
 atcacctgca gtgccagctc aagtataagt tccaattact tgcattggta tcagcagaag 120
 ccaggattct ccctaaact cttgatttat aggacatcca atctggcttc tggagtccca 180
 gtctgcttca gtggcagtgg gtctgggacc tcttactctc tcacaattgg caccatggag 240
 gctgaagatg ttgccactta ctactgccag cagggttaata gtataccatt cacgttcggc 300
 tcggggacaa agctcgag 318

<210> 17

<211> 134

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-k99 heavy chain variable region

<400> 17

Ala Thr Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Phe Val Lys
 1 5 10 15

Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 20 25 30

9

Ser Asp Tyr Phe Met Ser Trp Ile Arg Gln Thr Pro Glu Lys Arg Leu
 35 40 45

Glu Trp Val Ala Thr Ile Asn Asn Gly Gly Ser His Thr Tyr Cys Ser
 50 55 60

Asp Asn Val Lys Gly Arg Phe Thr Thr Phe Arg Asp Asn Val Lys Asn
 65 70 75 80

Thr Leu Tyr Leu Gln Met Ser Ser Leu Asn Phe Glu Asp Thr Ala Met
 85 90 95

Tyr Tyr Cys Ala Arg Ala Tyr Tyr Arg Phe Asp Val Arg Ala Trp Phe
 100 105 110

Ser Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr Ala Lys Thr
 115 120 125

Thr Pro Pro Ser Val Tyr
 130

<210> 18

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-k99 light chain

<220>

<221> MISC_FEATURE

<222> (225)..(226)

<223> X at positions 225 and 226 designates an unknown amino acid

<400> 18

Ala Thr Ser Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Met
 1 5 10 15

Ile Pro Arg Gln Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ile Ile
 20 25 30

10

Gly Thr Thr Ile His Trp Ser Gln Gln Arg Thr Asp Gly Ser Pro Arg
 35 40 45

Leu Leu Ile Gln Cys Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg
 50 55 60

Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Asn Phe Asn Ser
 65 70 75 80

Val Glu Ser Glu Tyr Ile Thr Asp Tyr Tyr Cys Gln Gln Ser Asn Thr
 85 90 95

Trp Pro Thr Tyr Pro Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 115 120 125

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 130 135 140

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 145 150 155 160

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 165 170 175

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 180 185 190

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
 195 200 205

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
 210 215 220

Xaa Xaa Thr Gly Phe
 225

<210> 19

<211> 29

<212> DNA

<213> Artificial Sequence

11

<220>

<223> Primer MLALT2

<400> 19

accatggatt ttcaagtgcg gatcttcag

29

<210> 20

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MLALT3

<400> 20

caccatggag wcacakwctc agtgcctttr t

31

<210> 21

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MLALT4

<400> 21

caccatgkcc ccwrctcagy tyctkgt

27

<210> 22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MLALT5

<400> 22

caccatgaag ttgcctgtta ggctgttg

28

12

<210> 23

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MH1

<400> 23

atatccacca tggratgsag ctgkgtmats ctctt

35

<210> 24

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MH2

<400> 24

atatccacca tgracttcgg gytgagctkg gtttt

35

<210> 25

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer 33615

<400> 25

gaagatctag acttactatg cagcatcagc

30

<210> 26

<211> 27

<212> DNA

<213> Artificial Sequence

13

<220>

<223> Primer MVG1R

<400> 26

ggcagcacta gtaggggccca gtggata

27

<210> 27

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer MVG2R

<400> 27

gaggarrccac tagtatctcc acacmcaggg gccag

35

<210> 28

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> ER transit peptide

<400> 28

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1 5 10 15

Ala Thr Ser

<210> 29

<211> 24

<212> DNA

<213> Artificial Sequence

14

<220>

<223> Primer

<400> 29

acgcgtcgat catccaggtg caac

24

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30

actagtggcg ctgcagcga ga

22

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 31

accggttctg ttctgcacaa agtgt

25

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 32

acgcgtttgt acccctggat t

21

15

<210> 33

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 33

acgcgtttgc atgcctgcag tg

22

<210> 34

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 34

agtccaacgg tggagcggaa ct

22

<210> 35

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> ER retention signal

<400> 35

Ser Glu Lys Asp Glu Leu

1

5

<210> 36

<211> 30

<212> DNA

16

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 36

agcttggatc cactagtacc ggtacgcgtg

30

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 37

aattcacgcg taccggtact agtggatcca

30

<210> 38

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 38

catgtgaggc caccacaag acctccacct ccccaatcgt gaagagcttc aaccgcaacg

60

agtgcgtgata ga

72

<210> 39

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

17

<223> Oligonucleotide

<400> 39

ccggtctatc agcactcggt gcggttgaag ctcttcacga ttggggaggt ggaggtcttg 60
tgggtggcct ca 72

<210> 40

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 40

agcttacgcg tggatccact agtgagctcg gtaccg 36

<210> 41

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 41

aattcgggtac cgagctcact agtggatcca cgcgta 36

<210> 42

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 42

ccgggcaagt ccgagaagga cgagctgtga taggagctca aggtaccgaa ttca 54

18

<210> 43

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 43

agcttgaatt cggtaaccttg agctcctatc acagctcgtc cttctcggac ttgc

54

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer IIA

<400> 44

aagcagtggg atcaacgcag agt

23

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer SMART IIA

<400> 45

aagcagtggg atcaacgcag agtacgcggg

30

<210> 46

<211> 22

<212> DNA

<213> Artificial Sequence

19

<220>

<223> Primer K99HC-3'

<400> 46

aagtagacag atgggggtgt cg

22

<210> 47

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_746_VAR_H5'

<400> 47

gccactagtg aagtgaagct tgaggag

27

<210> 48

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_1744_VAR_H5'

<400> 48

gccactagtg atgtgcagct ggtgga

26

<210> 49

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_3641_VAR_H5'

<400> 49

gccactagtg aggtccagct gcagcag

27

20

<210> 50

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_746_VAR_L5

<400> 50

ccactagtga aattgtgctc acccag

26

<210> 51

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_746_VAR_L3

<400> 51

ttatctcgag ctttgtcccc gagccgaa

28

<210> 52

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_3641_VAR_L5

<400> 52

gccactagtg aaaatgtgct caccag

27

<210> 53

<211> 28

<212> DNA

21

<213> Artificial Sequence

<220>

<223> Primer K88_3641_VAR_L3

<400> 53

ttatctcgag cttgggtgcct ccaccgaa

28

<210> 54

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_1744_VAR_L5

<400> 54

gccactagt acattgtgat gtcacag

27

<210> 55

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer K88_1744_VAR_L3

<400> 55

ttatctcgag cttgggtccca gcaccgaacg

30

<210> 56

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Light Chain Variable Domain Motif

22

<400> 56

Lys Leu Glu Ile Lys
 1 5

<210> 57

<211> 972

<212> DNA

<213> Artificial Sequence

<220>

<223> Consensus nucleotide sequence of murine IgG1 Heavy Chain

<400> 57

```

gccaaaacga ccccccatc tgtctatcca ctggccctg gatctgctgc ccaaactaac      60
tccatggatga ccctgggatg cctgggtcaag ggctatttcc ctgagccagt gacagtgacc      120
tggaactctg gatccctgtc cagcgggtgtg cacaccttcc cagctgtcct gcagtctgac      180
ctctacactc tgagcagctc agtgactgtc cctccagca cctggcccag cgagaccgtc      240
acctgcaacg ttgccacccc ggccagcagc accaagggtgg acaagaaaat tgtgcccagg      300
gatttgtggtt gtaagccttg catatgtaca gtcccagaag tatcatctgt cttcatcttc      360
ccccaaaagc ccaaggatgt gctcaccatt actctgactc ctaagggtcac gtgtgttgtg      420
gtagacatca gcaaggatga tcccagagtc cagttcagct ggtttgtaga tgatgtggag      480
gtgcacacag ctgagacgca accccgggag gagcagttca acagcacttt ccgctcagtc      540
agtgaacttc ccatcatgca ccaggactgg ctcaatggca aggagttcaa atgcagggtg      600
aacagtgcag ctttccctgc ccccatcgag aaaaccatct ccaaaaccaa aggcagaccg      660
aaggctccac aggtgtacac cattccacct cccaaggagc agatggccaa ggataaagtc      720
agtctgacct gcatgataac agacttcttc cctgaagaca ttactgtgga gtggcagtgg      780
aatgggcagc cagcggagaa ctacaagaac actcagccca tcatggacac agatggctct      840
tacttcgtct acagcaagct caatgtgcag aagagcaact gggaggcagg aaatactttc      900
acctgctctg tgttacatga gggcctgcac aaccaccata ctgagaagag cctctccac      960
tctcctggta aa

```

972

<210> 58

<211> 39

<212> DNA

23

<213> Artificial Sequence

<220>

<223> Primer for Human CH3

<400> 58

gaattaagga tccaaagcca aaggccagcc ccgcgaacc

39

<210> 59

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Human CH3

<400> 59

tttattgatt attgctcgag ttaccgccga gacagggga

38

<210> 60

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Murine CH3

<400> 60

aattaatgaa ttaaggatcc aagaccaagg gccgcccga gg

42

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Murine CH3

24

<400> 61

tttattgatt attgctcgag cttgcccggg gaggtagaga gg

42

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH3

<400> 62

aattaatgaa ttaaggatcc cgcaccaaag gccctgcc

38

<210> 63

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH3

<400> 63

tttattgatt attgctcgag cttgccggcg gacttggagg

40

<210> 64

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH2CH3

<400> 64

ttaatgaatt aaggatccgg cggcccatct gtgttcacat tc

42

<210> 65

<211> 40

25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer for Bovine CH2CH3

<400> 65

tttattgatt attgctcgag cttgccggcg gacttggagg

40

<210> 66

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence of IgG Fc sequences

<400> 66

His	Cys	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe
1				5					10					15	

Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
		20					25						30		

Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val
	35					40					45				

Gln	Pro	Val	Phe	Ser	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Thr	Ala
	50					55					60				

Lys	Met	Leu	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg
65					70					75				80	

Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
				85					90					95	

Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
			100					105						110	

Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Glu	Pro	Gln	Val
		115					120					125			

26

Tyr Val Leu Pro Pro Pro Arg Glu Glu Leu Ser Lys Asn Asp Thr Val
 130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile Ala Val
 145 150 155 160

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Asn Lys Tyr Lys Thr
 165 170 175

Thr Pro Pro Gln Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
 180 185 190

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Thr Phe Thr Cys
 195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 210 215 220

Ser Lys Ser Pro Gly Lys
 225 230

<210> 67

<211> 471

<212> PRT

<213> Mouse

<400> 67

Thr Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala
 1 5 10 15

Ser Ala Thr Ser Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
 20 25 30

Gln Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45

Phe Ser Ser Phe Ala Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
 50 55 60

Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Ser Ile Thr Ile Tyr Tyr
 65 70 75 80

Ala Asp Thr Val Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Pro Lys
 85 90 95

27

Ser Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala
 100 105 110

Met Tyr Tyr Cys Ala Arg Asp Asp Tyr Gly Ser Ser Gly Trp Tyr Phe
 115 120 125

Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr
 130 135 140

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
 145 150 155 160

Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu
 165 170 175

Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His
 180 185 190

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
 195 200 205

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
 210 215 220

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
 225 230 235 240

Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
 245 250 255

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
 260 265 270

Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp
 275 280 285

Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
 290 295 300

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser
 305 310 315 320

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
 325 330 335

28

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
 340 345 350

Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr
 355 360 365

Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
 370 375 380

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
 385 390 395 400

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
 405 410 415

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
 420 425 430

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
 435 440 445

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
 450 455 460

Lys Ser Glu Lys Asp Glu Leu
 465 470

<210> 68

<211> 244

<212> PRT

<213> Mouse

<400> 68

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

Ala Thr Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val
 20 25 30

Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu
 35 40 45

Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
 50 55 60

29

Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
 85 90 95
 Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr
 100 105 110
 Cys Thr Gln Ser Tyr Asn Leu Leu Thr Phe Gly Ala Gly Thr Lys Leu
 115 120 125
 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
 130 135 140
 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 145 150 155 160
 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 165 170 175
 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
 180 185 190
 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
 195 200 205
 Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
 210 215 220
 Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu
 225 230 235 240
 Lys Asp Glu Leu

<210> 69

<211> 469

<212> PRT

<213> Mouse

<400> 69

30

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

Ala Thr Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
 20 25 30

Thr Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Asp Tyr Ser Leu
 35 40 45

Thr Asp Tyr Tyr Met His Trp Val Lys Gln Ser His Gly Glu Ser Leu
 50 55 60

Glu Trp Ile Gly Tyr Ile Asn Phe Tyr Asn Gly Ala Thr Asn Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Phe Thr Val Asp Thr Ser Ser Ser
 85 90 95

Thr Val Tyr Met Gln Phe Asn Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Val Arg Glu Ala Leu Leu Arg Asn Tyr Ala Met Asp Tyr
 115 120 125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro
 130 135 140

Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser
 145 150 155 160

Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val
 165 170 175

Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe
 180 185 190

Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr
 195 200 205

Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
 210 215 220

His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp
 225 230 235 240

Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val
 245 250 255

31

Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr
 260 265 270
 Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu
 275 280 285
 Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln
 290 295 300
 Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser
 305 310 315 320
 Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys
 325 330 335
 Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile
 340 345 350
 Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro
 355 360 365
 Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met
 370 375 380
 Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn
 385 390 395 400
 Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr
 405 410 415
 Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn
 420 425 430
 Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu
 435 440 445
 His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ser
 450 455 460
 Glu Lys Asp Glu Leu
 465

<210> 70

<211> 240

32

<212> PRT

<213> mouse

<400> 70

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Glu Asn Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala
 20 25 30
 Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val
 35 40 45
 Ser Ser Arg Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro
 50 55 60
 Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
 85 90 95
 Ser Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser
 100 105 110
 Gly Tyr Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125
 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 130 135 140
 Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 145 150 155 160
 Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 165 170 175
 Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 180 185 190
 Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 195 200 205
 His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
 210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
 225 230 235 240

<210> 71

<211> 474

<212> PRT

<213> Mouse

<400> 71

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

Ala Thr Ser Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln
 20 25 30

Pro Gly Gly Ser Met Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Asn Tyr Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
 50 55 60

Glu Trp Val Ala Glu Ile Arg Leu Thr Ser Asn Asn Phe Ala Thr His
 65 70 75 80

Tyr Ala Glu Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser
 85 90 95

Lys Ser Ser Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr
 100 105 110

Gly Ile Tyr Tyr Cys Thr Arg Pro Tyr Tyr Gly Gly Arg Phe Phe Tyr
 115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
 130 135 140

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala
 145 150 155 160

Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 165 170 175

34

Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
 180 185 190

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 195 200 205

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val
 210 215 220

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 225 230 235 240

Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro
 245 250 255

Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
 260 265 270

Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
 275 280 285

Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu
 290 295 300

Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr
 305 310 315 320

Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn
 325 330 335

Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro
 340 345 350

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln
 355 360 365

Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val
 370 375 380

Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val
 385 390 395 400

Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln
 405 410 415

Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn
 420 425 430

35

Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val
 435 440 445

Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
 450 455 460

Ser Pro Gly Lys Ser Glu Lys Asp Glu Leu
 465 470

<210> 72

<211> 240

<212> PRT

<213> Mouse

<400> 72

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15

Ala Thr Ser Glu Ile Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala
 20 25 30

Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile
 35 40 45

Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro
 50 55 60

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Val
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly
 85 90 95

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Asn
 100 105 110

Ser Ile Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
 115 120 125

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
 130 135 140

36

Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
 145 150 155 160

Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
 165 170 175

Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
 180 185 190

Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
 195 200 205

His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
 210 215 220

Ile Val Lys Ser Phe Asn Arg Asn Glu Cys Ser Glu Lys Asp Glu Leu
 225 230 235 240

<210> 73

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 VL

<400> 73

Glu Asn Val Leu Thr Gln Ser Pro Ala Ile
 1 5 10

<210> 74

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 VL

<400> 74

Val Arg Leu Thr Gln Ser Pro Ala Ile
 1 5

37

<210> 75

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 VH

<400> 75

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu
1				5					10

<210> 76

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 VH

<400> 76

Glu	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu
1				5					10

<210> 77

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 derived VL produced in Cor
n

<400> 77

Glu	Asn	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ile
1				5					10

38

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 derived VL produced in Corn

<400> 78

Leu Val Leu Thr Gln Ser Pro Ala Ile
1 5

<210> 79

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted N-terminal sequence of 36/41 derived VH produced in Corn

<400> 79

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
1 5 10

<210> 80

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Obtained N-terminal sequence of 36/41 derived VH produced in Corn

<220>

<221> MISC_FEATURE

<222> (2)..(2)

39

<223> X at position 2 denotes that this residue was not obtained during sequencing

<400> 80

Glu	Xaa	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu
1			5						10